

0590  
0625 #6

OIIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/725,957

DATE: 11/21/2001

TIME: 10:21:58

Input Set : A:\ES.txt

Output Set: N:\CRF3\11212001\I725957.raw

P.5  
ENTERED

3 <110> APPLICANT: Her Majesty The Queen In Right Of Canada, As Represented By The  
Ministry  
4 Of Agriculture; Agri-Food Canada Both Of Canada Harris, Linda J.  
5 Gleddie, Stephen C.  
7 <120> TITLE OF INVENTION: Tolerance Of Trichothecene Mycotoxins In Plants Through The  
Modification  
8 Of The Ribosomal Protein L3 Gene  
10 <130> FILE REFERENCE: 08-874401US2  
12 <140> CURRENT APPLICATION NUMBER: US 09/725,957  
13 <141> CURRENT FILING DATE: 2000-11-30  
14 <150> PRIOR APPLICATION NUMBER: US 09/567,326  
15 <151> PRIOR FILING DATE: 2000-05-09  
17 <150> PRIOR APPLICATION NUMBER: US 08/909,828  
18 <151> PRIOR FILING DATE: 1997-08-12  
20 <160> NUMBER OF SEQ ID NOS: 18  
22 <170> SOFTWARE: PatentIn version 3.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 350  
26 <212> TYPE: PRT  
27 <213> ORGANISM: Saccharomyces cerevisiae (wild-type)  
29 <400> SEQUENCE: 1  
31 Met Ser His Arg Lys Tyr Glu Ala Pro Arg His Gly His Leu Gly Phe  
32 1 5 10 15  
34 Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe  
35 20 25 30  
37 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly  
38 35 40 45  
40 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly  
41 50 55 60  
43 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp  
44 65 70 75 80  
46 Thr Pro Pro Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro  
47 85 90 95  
49 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp  
50 100 105 110  
52 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys  
53 115 120 125  
55 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile  
56 130 135 140  
58 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val  
59 145 150 155 160  
61 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala  
62 165 170 175  
64 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val  
65 180 185 190  
67 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val  
68 195 200 205  
70 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His

71

210

215

220

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73 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
74 225                230                235                240
76 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His
77                245                250                255
79 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
80                260                265                270
82 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
83                275                280                285
85 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
86                290                295                300
88 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
89 305                310                315                320
91 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
92                325                330                335
94 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala
95                340                345                350
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 350
99 <212> TYPE: PRT
100 <213> ORGANISM: Saccharomyces cerevisiae (trichodermin-resistant)
102 <400> SEQUENCE: 2
104 Met Ser His Arg Lys Tyr Glu Ala Pro Arg His Gly His Leu Gly Phe
105 1                5                10                15
107 Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
108                20                25                30
110 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
111                35                40                45
113 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
114                50                55                60
116 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
117 65                70                75                80
119 Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
120                85                90                95
122 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
123                100                105                110
125 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
126                115                120                125
128 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
129                130                135                140
131 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
132 145                150                155                160
134 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
135                165                170                175
137 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
138                180                185                190
140 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
141                195                200                205
143 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
144                210                215                220

```

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Input Set : A:\ES.txt

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```

146 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
147 225                230                235                240
149 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Cys His
150                245                250                255
152 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
153                260                265                270
155 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
156                275                280                285
158 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
159                290                295                300
161 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
162 305                310                315                320
164 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
165                325                330                335
167 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala
168                340                345                350
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 389
172 <212> TYPE: PRT
173 <213> ORGANISM: Orzya sativa
175 <400> SEQUENCE: 3
177 Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
178 1                5                10                15
180 Leu Pro Arg Lys Arg Ser Ser Arg His Arg Gly Lys Val Lys Ser Phe
181                20                25                30
183 Pro Lys Asp Asp Val Ser Lys Pro Cys His Leu Thr Ser Phe Val Gly
184                35                40                45
186 Tyr Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
187 50                55                60
189 Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
190 65                70                75                80
192 Thr Pro Pro Leu Val Ile Val Gly Leu Val Ala Tyr Val Lys Thr Pro
193                85                90                95
195 Arg Gly Leu Arg Ser Leu Asn Ser Val Trp Ala Gln His Leu Ser Glu
196                100               105               110
198 Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
199                115               120               125
201 Ala Phe Thr Lys Tyr Ala Leu Lys Tyr Asp Ser Asp Ala Gly Lys Lys
202                130               135               140
204 Glu Ile Gln Met Gln Leu Glu Lys Met Lys Lys Tyr Ala Ser Ile Val
205 145               150               155               160
207 Arg Val Ile Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
208                165               170               175
210 Lys Lys Ala His Leu Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
211                180               185               190
213 Asp Lys Val Asp Tyr Gly Tyr Lys Phe Phe Glu Lys Glu Ile Pro Val
214                195               200               205
216 Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
217                210               215               220

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/725,957

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Input Set : A:\ES.txt

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```

219 Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
220 225                230                235                240
222 Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
223                245                250                255
225 Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
226                260                265                270
228 Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Ile
229                275                280                285
231 Gly Lys Ser Gly Gln Glu Ser His Ala Ala Cys Thr Glu Phe Asp Arg
232 290                295                300
234 Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
235 305                310                315                320
237 Val Lys Gly Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
238                325                330                335
240 Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Lys Gln Thr Ser Arg
241                340                345                350
243 Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ser Ser Lys
244                355                360                365
246 Phe Gly His Gly Arg Phe Gln Thr Thr Asp Glu Lys Gln Arg Phe Phe
247 370                375                380
249 Gly Lys Leu Lys Ala
250 385

```

252 &lt;210&gt; SEQ ID NO: 4

253 &lt;211&gt; LENGTH: 18

254 &lt;212&gt; TYPE: DNA

C--&gt; 255 &lt;213&gt; ORGANISM: Artificial

W--&gt; 256 &lt;220&gt; FEATURE:

257 &lt;223&gt; OTHER INFORMATION: Oligomer

259 &lt;400&gt; SEQUENCE: 4

260 ggctggatgg caggcacc

18

263 &lt;210&gt; SEQ ID NO: 5

264 &lt;211&gt; LENGTH: 18

265 &lt;212&gt; TYPE: DNA

C--&gt; 266 &lt;213&gt; ORGANISM: Artificial

W--&gt; 267 &lt;220&gt; FEATURE:

268 &lt;223&gt; OTHER INFORMATION: Primer

270 &lt;400&gt; SEQUENCE: 5

271 aagcgaccgt gcccgaaac

18

274 &lt;210&gt; SEQ ID NO: 6

275 &lt;211&gt; LENGTH: 18

276 &lt;212&gt; TYPE: DNA

C--&gt; 277 &lt;213&gt; ORGANISM: Artificial

W--&gt; 278 &lt;220&gt; FEATURE:

279 &lt;223&gt; OTHER INFORMATION: Primer

281 &lt;400&gt; SEQUENCE: 6

282 gtcgcacagg aagttcga

18

285 &lt;210&gt; SEQ ID NO: 7

286 &lt;211&gt; LENGTH: 1281

287 &lt;212&gt; TYPE: DNA

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TIME: 10:21:59

Input Set : A:\ES.txt

Output Set: N:\CRF3\11212001\I725957.raw

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288 <213> ORGANISM: Zea mays
290 <400> SEQUENCE: 7
291 atgtcgacaca ggaagttcga gcacccgagg cacggctccc tcggcttcct tcccaggaag      60
293 cgctcctccc gccaccgcgg caaggtgaag tcatttccca gggatgaccc caagaagcct      120
295 tgccatctca ctgccttcct tggctacaag gctggcatga ctacattgt ccgtgaggtt      180
297 gagaagccag gatccaaact ccataagaag gaaacttggt aggtgttac catcattgaa      240
299 accctcctc ttgtcattgt tgggctcgtg gcatatgtga agactcctcg tggcctccgc      300
301 acacccaact ctgtttgggc ccaacatctt agcgaagaag tgaggagaag gttctacaag      360
303 aactggtgca agagcaagaa gaaggctttc acaaagtatg ctctcaaata tgaaaatgat      420
305 gctggcaaga aggaaattca gctgcagctt gagaagatga agaaatatgc ttctgttatc      480
307 cgtgtcattg ctcataccca gattaggaag atgaagggtt tgaagcagaa gaaggctcac      540
309 ctgatggaga ttcaggtcaa tgggtgtacc attgctgaca aggtggacta tggctacaaa      600
311 ttttttgaga aagaggtccc tgttgatgct gtcttcaga aggatgagat gattgacatc      660
313 attggtgtga ccaaaggtaa aggttatgag ggtgtggtca ctcgttgggg tgtcaccgcg      720
315 cttccccgca aaaccacag gggctcctcg aaagtgtctt gtatcggtgc atggcatccg      780
317 gctagggctc cctatacggg tgcccgctgt ggtcagaatg ggtaccacca ccgactgag      840
319 atgaacaaga aggtctacaa gatcggcaag gctggacaag ggaccacga tgcctccaca      900
321 gagtttgaca ggaccgagaa ggacatcact cccatgggtg gcttccccca ctatggtatc      960
323 gtgaaggggt actacctgat gatcaagggc tgctgtgtgg gtccaaaaag aggggtggtg     1020
325 cctccgcca gtccctcctg aagcagactt cccggctggc gctggaggag atcaagctca     1080
327 agttcattga cacatcgtcc aagttcgggc acggtcgctt ccagactacc gatgagaagc     1140
329 agaggttctt tggcaagctc aaggcgtaag gtgctgcggt gcagcgaagt cccatttctc     1200
331 aaaatcatca aactgtgata cttttgtttg taacctgtct gtaccaagtt ttgtagccgg     1260
333 atggttcggg cacggtcgct t
336 <210> SEQ ID NO: 8
337 <211> LENGTH: 1282
338 <212> TYPE: DNA
339 <213> ORGANISM: Zea mays
341 <400> SEQUENCE: 8
342 atgtcgacaca ggaagttcga gcacccgagg cacggctccc tcggcttcct tcccaggaag      60
344 cgctcctccc gtcaccgcgg caaggtgaag tcattcccta gggatgaccc caagaagcct      120
346 tgccatctca ctgccttcct tggctacaag gctggcatga ctacattgt ccgtgaggtt      180
348 gagaagccag gatccaaact ccataagaag gaaacttggt aggtgttac catcattgaa      240
350 accctcctc ttgtcattgt tgggctcgtg gcatatgtga agactccccg tggcctccgc      300
352 aactcaact ctgtttgggc ccaacatctt agcgaagaag tgaggagaag gttctacaag      360
354 aactggtgca agagcaagaa gaaggctttc acaaagtatg ctctcaaata tgaaaatgat      420
356 gctggcaaga aggaaattca gctgcagctt gagaagatga agaaatatgc ttctgttatc      480
358 cgtgtcattg ctcataccca gattaggaag atgaagggtt tgaagcagaa gaaggctcac      540
360 ctgatggaga ttcaggtcaa tgggtgtacc attgctgaca aggtggacta tggctacaaa      600
362 ttctttgaga aagaggtccc tgttgatgct gtcttcaga aggatgagat gattgacatc      660
364 attggtgtga ccaaggggaa aggttatgag ggtgtggtca ctcgttgggg tgtcaccgcg      720
366 cttccccgca agaccacag gggctcctcg aaagtgtctt gtatcggtgc atggcatccg      780
368 gctagggctc cctatacggg tgctcgtgct ggtcagaatg ggtaccacca ccgactgag      840
370 atgaacaaga aggtttacaa gatcggcaag gctggacaag agaccacga tgcctccaca      900
372 gagtttgaca ggactgagaa ggacatcact cccatgggtg gcttccccca ttatggtatc      960
374 gtgaaggggt actacctgat gatcaagggc tgctgtgtgg gtccaaagaa gaggggtggtg     1020
376 accctccgcc agtccctcct gaagcagact tcccggctgg cgtgaggga gatcaagctc     1080
378 aagttcctcg acacatcgtc caagttcggg cacggtcgct tccagactac cgatgagaag     1140
380 cagaggttct ttggcaagct caaggcgtaa ggtgctgcgg tgcagcgaag tcccatttct     1200

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 11/21/2001

PATENT APPLICATION: US/09/725,957

TIME: 10:22:00

Input Set : A:\ES.txt

Output Set: N:\CRF3\11212001\I725957.raw

L:255 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:256 M:283 W: Missing Blank Line separator, <220> field identifier  
L:266 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:267 M:283 W: Missing Blank Line separator, <220> field identifier  
L:277 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:278 M:283 W: Missing Blank Line separator, <220> field identifier  
L:942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17